

GenCore version 5.1.3  
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OM protein - protein search, using sw med-4

Run on: January 2, 2003, 11:41:31, Search time 18 seconds  
(without alignments)  
1591.559 Million cell updates/sec

Title: US-09-185-904A-33  
Perfect score: 1543  
Sequence: 1 MTPQALSPKALPLAGGIAAA IPRG75AEVIVYVLEKKVL 298

Scoring table: PROGM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 9613442 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DE seq length: 0

Maximum DE seq length: 200000000

Post-processing: Minimum Match 48

Listing first 45 summaries

Database: PIR-73:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pres. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	LC	Description
1	1543	100.0	299	1	509943	ADP, ATP carrier pr
2	1512	99.0	298	1	843646	ADP, ATP carrier pr
3	1454	94.2	298	1	829132	ADP, ATP carrier pr
4	1421	92.3	298	2	160173	ADP, ATP carrier pr
5	1422	92.2	298	2	8685	ADP, ATP carrier pr
6	1418	91.9	298	2	837210	ADP, ATP carrier pr
7	1409	91.3	294	2	811778	ADP, ATP carrier pr
8	1407	91.1	296	2	831814	ADP, ATP carrier pr
9	1184	76.7	301	1	831826	ADP, ATP carrier pr
10	1041	67.5	313	2	123207	hypothetical prote
11	1019	67.2	313	2	123208	hypothetical prote
12	1028	67.3	300	2	837210	hypothetical prote
13	993.6	64.4	300	2	115206	hypothetical prote
14	978	63.4	339	2	841677	ADP, ATP carrier pr
15	943	61.1	301	2	851132	ADP, ATP carrier pr
16	778.5	50.5	307	2	836597	ADP, ATP carrier pr
17	772	50.0	308	1	830259	ADP, ATP carrier pr
18	763	49.8	322	2	110755	ADP, ATP carrier pr
19	768	49.8	386	2	109709	ADP, ATP carrier pr
20	765	49.6	310	1	8685	ADP, ATP carrier pr
21	764	49.5	334	2	125728	hypothetical prote
22	742.5	49.1	307	2	859151	ADP, ATP carrier pr
23	740.5	49.3	318	1	831978	ADP, ATP carrier pr
24	745.6	49.3	336	1	120912	hypothetical prote
25	759	48.6	397	2	814876	ADP, ATP carrier pr
26	742	48.5	383	2	851971	ADP, ATP carrier pr
27	747	48.4	386	2	142011	ADP, ATP carrier pr
28	747	48.4	386	2	837917	ADP, ATP carrier pr
29	744	48.2	387	2	816568	ADP, ATP carrier pr

30	742	48.2	379	1	104598	ADP, ATP carrier pr
31	742.5	48.1	385	1	829872	ADP, ATP carrier pr
32	742	48.1	382	2	833530	ADP, ATP carrier pr
33	739.5	47.9	386	2	814874	ADP, ATP carrier pr
34	737.5	47.8	309	2	824819	ADP, ATP carrier pr
35	734.5	47.6	379	2	821313	ADP, ATP carrier pr
36	691.5	44.2	298	2	124039	hypothetical prote
37	520.5	33.7	327	2	121577	ADP, ATP carrier pr
38	383	24.8	325	2	104273	hypothetical prote
39	381	24.7	352	2	101729	mitochondrial solu
40	372	24.1	358	2	145934	hypothetical prote
41	370.5	24.0	415	2	148171	hypothetical prote
42	369.5	23.9	381	2	151158	hypothetical prote
43	368	23.8	475	2	150636	peroxisomal Ca-dep
44	363	23.5	348	2	184738	probable mitochond
45	344.5	22.3	332	2	184733	Ca-dependent solut

ALIGNMENTS

RESULT 1  
S03894  
ADP, ATP carrier protein T3 - human  
N: Alternate names: ADP, ATP carrier protein T2 (misidentification); mitochondrial A  
C: Species: Homo sapiens (man)  
C: Date: 27 Mar 2003; accession: 17-Mar-2003; atox\_date: 17-Mar-2000  
C: Accession: S03894; B28116  
R: Cozens, A.L.; Runswick, M.J.; Walker, J.E.  
J. Mol. Biol. 206, 261-280, 1989  
A: Title: DNA sequences of two expressed nuclear genes for human mitochondrial A  
A: Reference number: S03894; M010802330; F010251251  
A: Accession: S03894  
A: Status: not compared with conceptual translation  
A: Molecule type: DNA  
A: Residues: 1-298-302  
F: Residues: 1-298-302  
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
A: Title: Two distinct genes for ADP/ATP translocase are expressed at the mRN level  
A: Reference number: A94297; M0108121845; F0102829183  
A: Accession: B28116  
A: Molecule type: mRNA  
A: Residues: 1-113-113  
A: Cross-reference: G0103500; N01039702; M010833650; F010397023  
A: Experimental source: liver  
C: Genetics:  
A: Gene: GDB: ANT3; ANT3Y  
A: Cross-references: G0103500; M010833650; M010840000  
A: Map position: A022357; p11.13  
A: Note: there may be some confusion in the assignment of sequences for GDB: ANT3  
A: Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology  
A: Keywords: duplicated; homodimer; mitochondrial; transmembrane protein  
A: 258/258; predicted; ADP, ATP carrier protein; status: predicted; MAN  
A: 258/258; ADP, ATP carrier protein; repeat homology; ACPI  
A: 113/292; ADP, ATP carrier protein; repeat homology; ACPI  
A: 258/258; ADP, ATP carrier protein; repeat homology; ACPI

Query Match	100.0%	Score	354.5	DB 1	Length	386			
Best Local Similarity	100.0%	Each Res	6.129						
Matches	298	Conserved	0	Mismatches	0	Gaps	0		
30	1	MTQALSPKALPLAGGIAAA	SEPTAVATTEVFTELVCHAEFLTAAPQYR	INACTIVE	60				
100	1	MTQALSPKALPLAGGIAAA	ISKIAVAP	IPVKIL	IIQWASKIAAUKQYKGI	VDCLVR	60		
30	61	ITTFQSV	STWSTN	ANVTFTPTQAN	NFATFYSKEL	FTGVPHIT	SIWEY	ACNLASG	120
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120	61	ITTFQSV	STWSTN	ANVTFTPTQAN	NFATFYSKEL	FTGVPHIT	SIWEY	ACNLASG	120
120	61	ITTFQSV	STWSTN	ANVTFTPTQAN	NFATFYSKEL	FTGVPHIT	SIWEY	ACNLASG	120
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99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 1118 1119 1120 1121 1122 1123 1124 1125 1126 1127 1128 1129 1130 1131 1132 1133 1134 1135 1136 1137 1138 1139 1140 1141 1142 1143 1144 1145 1146 1147 1148 1149 1150 1151 1152 1153 1154 1155 1156 1157 1158 1159 1160 1161 1162 1163 1164 1165 1166 1167 1168 1169 1170 1171 1172 1173 1174 1175 1176 1177 1178 1179 1180 1181 1182 1183 1184 1185 1186 1187 1188 1189 1190 1191 1192 1193 1194 1195 1196 1197 1198 1199 1200 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1401 1402 1403 1404 1405 1406 1407 1408 1409 1410 1411 1412 1413 1414 1415 1416 1417 1418 1419 1420 1421 1422 1423 1424 1425 1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438 1439 1440 1441 1442 1443 1444 1445 1446 1447 1448 1449 1450 1451 1452 1453 1454 1455 1456 1457 1458 1459 1460 1461 1462 1463 1464 1465 1466 1467 1468 1469 1470 1471 1472 1473 1474 1475 1476 1477 1478 1479 1480 1481 1482 1483 1484 1485 1486 1487 1488 1489 1490 1491 1492 1493 1494 1495 1496 1497 1498 1499 1500 1501 1502 1503 1504 1505 1506 1507 1508 1509 1510 1511 1512 1513 1514 1515 1516 1517 1518 1519 1520 1521 1522 1523 1524 1525 1526 1527 1528 1529 1530 1531 1532 1533 1534 1535 1536 1537 1538 1539 1540 1541 1542 1543 1544 1545 1546 1547 1548 1549 1550 1551 1552 1553 1554 1555 1556 1557 1558 1559 1560 1561 1562 1563 1564 1565 1566 1567 1568 1569 1570 1571 1572 1573 1574 1575 1576 1577 1578 1579 1580 1581 1582 1583 1584 1585 1586 1587 1588 1589 1590 1591 1592 1593 1594 1595 1596 1597 1598 1599 1600 1601 1602 1603 1604 1605 1606 1607 1608 1609 1610 1611 1612 1613 1614 1615 1616 1617 1618 1619 1620 1621 1622 1623 1624 1625 1626 1627 1628 1629 1630 1631 1632 1633 1634 1635 1636 1637 1638 1639 1640 1641 1642 1643 1644 1645 1646 1647 1648 1649 1650 1651 1652 1653 1654 1655 1656 1657 1658 1659 1660 1661 1662 1663 1664 1665 1666 1667 1668 1669 1670 1671 1672 1673 1674 1675 1676 1677 1678 1679 1680 1681 1682 1683 1684 1685 1686 1687 1688 1689 1690 1691 1692 1693 1694 1695 1696 1697 1698 1699 1700 1701 1702 1703 1704 1705 1706 1707 1708 1709 1710 1711 1712 1713 1714 1715 1716 1717 1718 1719 1720 1721 1722 1723 1724 1725 1726 1727 1728 1729 1730 1731 1732 1733 1734 1735 1736 1737 1738 1739 1740 1741 1742 1743 1744 1745 1746 1747 1748 1749 1750 1751 1752 1753 1754 1755 1756 1757 1758 1759 1760 1761 1762 1763 1764 1765 1766 1767 1768 1769 1770 1771 1772 1773 1774 1775 1776 1777 1778 1779 1780 1781 1782 1783 1784 1785 1786 1787 1788 1789 1790 1791 1792 1793 1794 1795 1796 1797 1798 1799 1800 1801 1802 1803 1804 1805 1806 1807 1808 1809 1810 1811 1812 1813 1814 1815 1816 1817 1818 1819 1820 1821 1822 1823 1824 1825 1826 1827 1828 1829 1830 1831 1832 1833 1834 1835 1836 1837 1838 1839 1840 1841 1842 1843 1844 1845 1846 1847 1848 1849 1850 1851 1852 1853 1854 1855 1856 1857 1858 1859 1860 1861 1862 1863 1864 1865 1866 1867 1868 1869 1870 1871 1872 1873 1874 1875 1876 1877 1878 1879 1880 1881 1882 1883 1884 1885 1886 1887 1888 1889 1890 1891 1892 1893 1894 1895 1896 1897 1898 1899 1900 1901 1902 1903 1904 1905 1906 1907 1908 1909 1910 1911 1912 1913 1914 1915 1916 1917 1918 1919 1920 1921 1922 1923 1924 1925 1926 1927 1928 1929 1930 1931 1932 1933 1934 1935 1936 1937 1938 1939 1940 1941 1942 1943 1944 1945 1946 1947 1948 1949 1950 1951 1952 1953 1954 1955 1956 1957 1958 1959 1960 1961 1962 1963 1964 1965 1966 1967 1968 1969 1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 271















us-09-185-904a-33.rsp

Fri Jan 3 10:31:14 2003

075746 homo sapien  
P16261 rattus norv  
Q21153 caenorhabdi  
G95258 homo sapien  
P16260 mus musculu  
Q92262 mus musculu  
Q13805 schizosacch  
Q94350 homo sapien  
Q942d1 homo sapien  
P55916 homo sapien  
Q94xx4 mus musculu

34 395 19.1 678 1 CMC1\_HUMAN  
35 285.5 18.8 322 1 GDC\_RAT  
36 287.5 18.6 702 1 CMC1\_CAEFL  
37 386 18.5 325 1 HCP5\_HUMAN  
38 284 18.4 325 1 HCP5\_HUMAN  
39 284 18.4 325 1 UCP5\_MOUSE  
40 282.5 18.3 324 1 YF08\_SC4PO  
41 280 18.1 675 1 CMC2\_HUMAN  
42 272 17.5 315 1 MPT\_HUMAN  
43 276 17.4 315 1 SATR\_HUMAN  
44 265 17.2 312 1 UCP3\_HUMAN  
45 265 17.2 676 1 CMC2\_MOUSE

ADP3\_HUMAN  
ID ADP3\_HUMAN STANDARD: PRT: 298 AA.  
AC P12236: Q96C49;  
DI 01-06-1989 (rel. 12, Last sequence update)  
DI 01-NOV-1990 (rel. 16, Last annotation update)  
DI 15-JUN-2002 (rel. 41, Last annotation update)  
DE ADP/ATP carrier protein, liver isoform 12 (ADP/ATP translocase 3)  
DE (Adenine nucleotide translocator 3) (ANT 3).  
GN SLC25A6 OR ANT3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RF MEDLINE:89476376; PubMed:2541251;  
RA Coziers A.L., Ruswick M.J., Walker J.E.;  
RT "DNA sequences of two expressed nuclear genes for human mitochondrial  
ADP/ATP translocase.";  
RL J. Mol. Biol. 206:261-280(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,  
Margolin J.P.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA TISSUE:Brain, Cervix, Eye, and Lung;  
RL Strausberg R.;  
RN Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases  
RA [4]  
RP SEQUENCE OF 36 298 FROM N.A.  
RA TISSUE:Liver;  
RA MGI:0121845; PubMed:254183;  
RA Houldsworth J., Attardi G.;  
RP "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
level in adult human liver.";  
ET Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
RL FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
CC -1- MITOCHONDRIAL INNER MEMBRANE  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC -1- SUBUNIT: HOMO-DIMER.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
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CC or send an email to [license@isb.sib.ch](mailto:license@isb.sib.ch)).  
CC EMBL: J03592; AAA:56750.1;  
CC

# ALIGNMENTS

## RESULT 1

ADP3\_HUMAN  
ID ADP3\_HUMAN STANDARD: PRT: 298 AA.  
AC P12236: Q96C49;  
DI 01-06-1989 (rel. 12, Last sequence update)  
DI 01-NOV-1990 (rel. 16, Last annotation update)  
DI 15-JUN-2002 (rel. 41, Last annotation update)  
DE ADP/ATP carrier protein, liver isoform 12 (ADP/ATP translocase 3)  
DE (Adenine nucleotide translocator 3) (ANT 3).  
GN SLC25A6 OR ANT3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RF MEDLINE:89476376; PubMed:2541251;  
RA Coziers A.L., Ruswick M.J., Walker J.E.;  
RT "DNA sequences of two expressed nuclear genes for human mitochondrial  
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RL J. Mol. Biol. 206:261-280(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,  
Margolin J.P.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA TISSUE:Brain, Cervix, Eye, and Lung;  
RL Strausberg R.;  
RN Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases  
RA [4]  
RP SEQUENCE OF 36 298 FROM N.A.  
RA TISSUE:Liver;  
RA MGI:0121845; PubMed:254183;  
RA Houldsworth J., Attardi G.;  
RP "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
level in adult human liver.";  
ET Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
RL FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
CC -1- MITOCHONDRIAL INNER MEMBRANE  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC -1- SUBUNIT: HOMO-DIMER.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
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CC or send an email to [license@isb.sib.ch](mailto:license@isb.sib.ch)).  
CC EMBL: J03592; AAA:56750.1;  
CC

GenCore version 5.1.3  
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AM protein - protein search, using sw model

Run on: January 2, 2003, 14:20:21 ; Search time 14 seconds

(without alignments)  
892.953 Million cell updates/sec

Title: US-09-185-904A-33

Perfect score: 1543

Sequence: 1 MTEQMTSFADFLAAGTAA...LRMGAFVLVLYDELKKVI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 6

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pled. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	ADP3_HUMAN	P12236 homo sapien
2	1512	98.0	298	ADT3_BOVIN	P32097 bos taurus
3	1453	94.8	298	ADT2_HUMAN	P05141 homo sapien
4	1451	94.0	298	ADT2_PAT	Q09073 rattus norv
5	1445	93.6	298	ADT2_MOUSE	P51881 mus musculu
6	1424	92.3	298	ADT1_RAT	Q05962 rattus norv
7	1418	91.9	298	ADT1_MOUSE	P44962 mus musculu
8	1417	91.8	297	ADT1_HUMAN	P02722 bos taurus
9	1409	91.3	298	ADT1_HUMAN	P12235 homo sapien
10	1217.5	78.9	297	ADT1_DROME	Q26365 drosophila
11	1204	78.0	301	ADT1_AROJA	P07244 anopheles g
12	778	63.4	319	ADT1_CHLKE	P16692 chlorella k
13	772	50.5	307	ADT3_YEAST	P18238 saccharomy
14	772	50.0	308	ADT1_CHLFE	P27080 chlamydomon
15	765	49.8	322	ADT1_SCHPC	Q09188 schizosacch
16	765	49.8	386	ADT1_GOSHI	C22342 gossypium h
17	765	49.6	313	ADT1_NEUTP	P27273 neuropeptid
18	752.5	49.4	355	ADT1_KLIFA	P19382 kluyveromy
19	750.5	49.3	318	ADT2_YEAST	P18239 saccharomy
20	750.5	48.6	385	ADT2_ARATH	P40941 arabidopsis
21	750.5	48.6	387	ADT1_MAIZE	P04709 oca mayz (m
22	748	48.5	386	ADT1_SOLFO	P25083 solanum tub
23	747	48.4	392	ADT1_ORYSA	P31691 oryza sativ
24	744	48.2	387	ADT2_MAIZE	P12857 oca mayz (m
25	742.5	48.1	381	ADT1_ARATH	P31167 arabidopsis
26	740	48.0	331	ADT1_WHEAT	P41629 triticum ae
27	739.5	47.9	386	ADT2_SGCTO	P27081 solanum tub
28	737.5	47.8	309	ADT1_YEAST	P04710 saccharomy
29	727	47.1	331	ADT2_WHEAT	Q41630 triticum ae
30	727	47.1	588	CMC2_CAEFL	Q26739 caenorhabd
31	700	19.6	430	GDC_BOVIN	Q01888 bos taurus
32	299	19.4	407	GDC_RAT	G99297 saccharomy
33	297	19.2	587	CMC3_CAEFL	Q19529 caenorhabd



us-09-185-904a-33.rsp

Fri Jan 3 10:31:14 2003

ADP/ATP carrier protein, fibroblast isoform (ADP/ATP Translocase 2)  
 (Adenine nucleotide translocator 2) (ANT 2).  
 G1 5225A5; Cf ANT2.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID: 9606;  
 RN [1] J. Biol. Chem. 265:16060-16063 (1990).  
 RP SEQUENCE FROM N.A.  
 RC TISSUE: Placenta;  
 KA Molecular Weight: 27,500; pI: 5.3-5.6; pKa: 7.2  
 RA Ka D. H., Kadan J., Chen S.-T., Chang C.-D., Baserga W., Wurzel J.;  
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular  
 cloning and sequence".  
 RL J. Biol. Chem. 265:16060-16063 (1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE 97166056; PubMed=4041073;  
 RA Battini R., Ferrari S., Kozlowski L., Calabretta B., Chen S.-T.,  
 RA Baserga W.;  
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is  
 K1 involved in regulation of cellular energy metabolism".  
 RL J. Biol. Chem. 262:4355-4358 (1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 KA Chen S.-T., Kadan J., Baserga W., Wurzel J.,  
 RA Mazzarella R.A., Schlessinger D., Chen S.-T.;  
 RL Submitted (Jun 1990) to the EMBL/GenBank/DDBJ databases  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 KA Chen S.-T., Kadan J., Baserga W., Wurzel J.,  
 RA Mazzarella R.A., Schlessinger D., Chen S.-T.;  
 RL Submitted (Jun 1990) to the EMBL/GenBank/DDBJ databases  
 RN [5]  
 RP SEQUENCE OF 47 298 FROM N.A.  
 RC TISSUE: Liver;  
 KA Molecular Weight: 27,500; pI: 5.3-5.6; pKa: 7.2  
 RA Bouldsworth J., Attardi G.;  
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA  
 level in adult human liver".  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 inner membrane.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
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 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).  
 DR EMBL: M7121; AAA35777.1;  
 DR EMBL: J02683; AAA35579.1;  
 DR EMBL: U78810; AAH39246.1;  
 DR EMBL: AC004000; AAB96347.1;  
 DR EMBL: J03591; AAA36749.1;  
 DR EMBL: A25132; A29132.  
 DR PIR: C28116; C28116;  
 DR Gene: HNC1099; S 02655  
 DR MIM: 300150;  
 DR InterPro: IPR000067; Mit\_carrier  
 DR InterPro: IPR001993; Mitoch carrier.  
 DR Pfam: PF00153; mito\_carrier\_3.  
 DR PRINTS: PR00925; MIT\_CARRIER.  
 DR PROSITE: PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 FT TRANSMEM 12 29 1 (POTENTIAL).

FT TRANSMEM 73 91 2 (POTENTIAL).  
 FT TRANSMEM 117 134 3 (POTENTIAL).  
 FT TRANSMEM 176 195 4 (POTENTIAL).  
 FT TRANSMEM 214 231 5 (POTENTIAL).  
 FT TRANSMEM 273 291 6 (POTENTIAL).  
 FT REPEAT 1 111 1.  
 FT REPEAT 112 208 2.  
 FT REPEAT 209 298 3.  
 FT CONFLICT 6 V -> L (IN REF. 2).  
 FT CONFLICT 66 G -> E (IN REF. 2).  
 FT CONFLICT 111 R -> L (IN REF. 4 AND 5).  
 FT CONFLICT 162 V -> S (IN REF. 5).  
 SQ SEQUENCE 298 AA: 12895 MW: 19730.342 Da; 298 AA: 12895 MW: 19730.342 Da; 298 AA: 12895 MW: 19730.342 Da;  
 Query Match 94.88; Score 1463; DB 1; Length 298;  
 Res. Local Similarity 92.4%; Proj. No. 6.9e123;  
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;  
 OY 1 MTEQATSEAFKDFLAGGIAAISKTAIVAPIERVKLLQVQIASKQIAADKQYK; VDCIVR 60  
 DB 1 MTDAAVSPKDFLAGGVAIAISKTAIVAPIERVKLLQVQIASKQIADKQYK; IDCIVR 60  
 OY 51 LKFTGVYLSIWRGLANVIFPTQA-NPAFKDKYKQIFLGSGYDKKHPTQWRYFAGNLSG 120  
 DB 51 LKFTGVYLSIWRGLANVIFPTQA-NPAFKDKYKQIFLGSGYDKKHPTQWRYFAGNLSG 120  
 OY 121 GAAGATSLKLVYVLDFAPTFLAAYVSKSTERTERGLDGLIVLTKSNGIKGLQGFVS 180  
 DB 121 GAAGATSLKLVYVLDFAPTFLAAYVSKSTERTERGLDGLIVLTKSNGIKGLQGFVS 180  
 OY 181 VQGIITVRAAYFGVYDTAKGMLDPPKNTHTVWSNMIAGTAVAGVSYPPDTVRRMM 240  
 DB 181 VQGIITVRAAYFGVYDTAKGMLDPPKNTHTVWSNMIAGTAVAGVSYPPDTVRRMM 240  
 OY 241 QSGKKGALDVTGTVCWPKTPPDEQKAFKSGAWSNVLRGSGAFVLYVDELKK 296  
 DB 241 QSGKKGALDVTGTVCWPKTPPDEQKAFKSGAWSNVLRGSGAFVLYVDELKK 296  
 RESULT 4  
 ADP2\_RAT SLANLRL EST. 298 AA.  
 AC Q09673;  
 DT 01 FEB 1995 (rel. 31, Created)  
 DT 01 FEB 1995 (rel. 31, Last sequence update)  
 DT 16 OCT 2001 (rel. 40, Last annotation update)  
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)  
 DE (Adenine nucleotide translocator 2) (ANT 2).  
 EN Rattus norvegicus (Rat).  
 EN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 EN Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 EN NCBI\_TaxID: 10116.  
 EN [1]  
 EN SEQUENCE FROM N.A.  
 EN TISSUE: Liver;  
 EN MEDLINE 94002151; PubMed=8499300;  
 EN Shiohara Y., Kamada M., Yamazaki N., Terada H.;  
 EN "Isolation and characterization of cDNA clones and a genomic clone  
 encoding rat mitochondrial adenine nucleotide translocator".  
 EN Biochim. Biophys. Acta 1152:192-196 (1993).  
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE  
 CC MITOCHONDRIAL INNER MEMBRANE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
 CC inner membrane.  
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND  
 CC SKELETAL MUSCLE.  
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
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 DR EMBL: M7121; AAA35777.1;  
 DR EMBL: J02683; AAA35579.1;  
 DR EMBL: U78810; AAH39246.1;  
 DR EMBL: AC004000; AAB96347.1;  
 DR EMBL: J03591; AAA36749.1;  
 DR EMBL: A25132; A29132.  
 DR PIR: C28116; C28116;  
 DR Gene: HNC1099; S 02655  
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 DR InterPro: IPR000067; Mit\_carrier  
 DR InterPro: IPR001993; Mitoch carrier.  
 DR Pfam: PF00153; mito\_carrier\_3.  
 DR PRINTS: PR00925; MIT\_CARRIER.  
 DR PROSITE: PS00215; MITOCH\_CARRIER; 3.  
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;  
 FT TRANSMEM 12 29 1 (POTENTIAL).

the value of the probability of the event  $A$  is equal to the value of the probability of the event  $\bar{A}$  (the complement of the event  $A$ ), that is,  $P(A) = P(\bar{A})$ . The probability of the event  $A$  is equal to the probability of the event  $\bar{A}$  if and only if the event  $A$  is a certain event, that is,  $P(A) = 1$  and  $P(\bar{A}) = 0$ . The probability of the event  $A$  is equal to the probability of the event  $\bar{A}$  if and only if the event  $A$  is a certain event, that is,  $P(A) = 1$  and  $P(\bar{A}) = 0$ . The probability of the event  $A$  is equal to the probability of the event  $\bar{A}$  if and only if the event  $A$  is a certain event, that is,  $P(A) = 1$  and  $P(\bar{A}) = 0$ .

[illegible]

Run	Sample	Time (hr)	Yield (%)	Analysis
1	TRANS-MEM	1.7	2.9	C, 60.0 (CALC); H, 4.0 (CALC)
2	TRANS-MEM	3.4	3.4	C, 60.0 (CALC); H, 4.0 (CALC)
3	TRANS-MEM	1.7	3.4	C, 60.0 (CALC); H, 4.0 (CALC)
4	TRANS-MEM	1.7	3.4	C, 60.0 (CALC); H, 4.0 (CALC)
5	TRANS-MEM	1.4	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
6	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
7	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
8	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
9	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
10	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
11	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
12	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
13	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
14	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
15	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
16	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
17	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
18	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
19	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)
20	TRANS-MEM	1.7	4.1	C, 60.0 (CALC); H, 4.0 (CALC)

Country	March	Oct. 1978	Sept. 1979	Feb. 1980	Sept. 1980	Oct. 1980	Nov. 1980	Dec. 1980	Jan. 1981	Feb. 1981	Mar. 1981	Apr. 1981	May 1981	June 1981	July 1981	Aug. 1981	Sept. 1981	Oct. 1981	Nov. 1981	Dec. 1981	Jan. 1982	Feb. 1982	Mar. 1982	Apr. 1982	May 1982	June 1982	July 1982	Aug. 1982	Sept. 1982	Oct. 1982	Nov. 1982	Dec. 1982	Jan. 1983	Feb. 1983	Mar. 1983	Apr. 1983	May 1983	June 1983	July 1983	Aug. 1983	Sept. 1983	Oct. 1983	Nov. 1983	Dec. 1983	Jan. 1984	Feb. 1984	Mar. 1984	Apr. 1984	May 1984	June 1984	July 1984	Aug. 1984	Sept. 1984	Oct. 1984	Nov. 1984	Dec. 1984	Jan. 1985	Feb. 1985	Mar. 1985	Apr. 1985	May 1985	June 1985	July 1985	Aug. 1985	Sept. 1985	Oct. 1985	Nov. 1985	Dec. 1985	Jan. 1986	Feb. 1986	Mar. 1986	Apr. 1986	May 1986	June 1986	July 1986	Aug. 1986	Sept. 1986	Oct. 1986	Nov. 1986	Dec. 1986	Jan. 1987	Feb. 1987	Mar. 1987	Apr. 1987	May 1987	June 1987	July 1987	Aug. 1987	Sept. 1987	Oct. 1987	Nov. 1987	Dec. 1987	Jan. 1988	Feb. 1988	Mar. 1988	Apr. 1988	May 1988	June 1988	July 1988	Aug. 1988	Sept. 1988	Oct. 1988	Nov. 1988	Dec. 1988	Jan. 1989	Feb. 1989	Mar. 1989	Apr. 1989	May 1989	June 1989	July 1989	Aug. 1989	Sept. 1989	Oct. 1989	Nov. 1989	Dec. 1989	Jan. 1990	Feb. 1990	Mar. 1990	Apr. 1990	May 1990	June 1990	July 1990	Aug. 1990	Sept. 1990	Oct. 1990	Nov. 1990	Dec. 1990	Jan. 1991	Feb. 1991	Mar. 1991	Apr. 1991	May 1991	June 1991	July 1991	Aug. 1991	Sept. 1991	Oct. 1991	Nov. 1991	Dec. 1991	Jan. 1992	Feb. 1992	Mar. 1992	Apr. 1992	May 1992	June 1992	July 1992	Aug. 1992	Sept. 1992	Oct. 1992	Nov. 1992	Dec. 1992	Jan. 1993	Feb. 1993	Mar. 1993	Apr. 1993	May 1993	June 1993	July 1993	Aug. 1993	Sept. 1993	Oct. 1993	Nov. 1993	Dec. 1993	Jan. 1994	Feb. 1994	Mar. 1994	Apr. 1994	May 1994	June 1994	July 1994	Aug. 1994	Sept. 1994	Oct. 1994	Nov. 1994	Dec. 1994	Jan. 1995	Feb. 1995	Mar. 1995	Apr. 1995	May 1995	June 1995	July 1995	Aug. 1995	Sept. 1995	Oct. 1995	Nov. 1995	Dec. 1995	Jan. 1996	Feb. 1996	Mar. 1996	Apr. 1996	May 1996	June 1996	July 1996	Aug. 1996	Sept. 1996	Oct. 1996	Nov. 1996	Dec. 1996	Jan. 1997	Feb. 1997	Mar. 1997	Apr. 1997	May 1997	June 1997	July 1997	Aug. 1997	Sept. 1997	Oct. 1997	Nov. 1997	Dec. 1997	Jan. 1998	Feb. 1998	Mar. 1998	Apr. 1998	May 1998	June 1998	July 1998	Aug. 1998	Sept. 1998	Oct. 1998	Nov. 1998	Dec. 1998	Jan. 1999	Feb. 1999	Mar. 1999	Apr. 1999	May 1999	June 1999	July 1999	Aug. 1999	Sept. 1999	Oct. 1999	Nov. 1999	Dec. 1999	Jan. 2000	Feb. 2000	Mar. 2000	Apr. 2000	May 2000	June 2000	July 2000	Aug. 2000	Sept. 2000	Oct. 2000	Nov. 2000	Dec. 2000	Jan. 2001	Feb. 2001	Mar. 2001	Apr. 2001	May 2001	June 2001	July 2001	Aug. 2001	Sept. 2001	Oct. 2001	Nov. 2001	Dec. 2001	Jan. 2002	Feb. 2002	Mar. 2002	Apr. 2002	May 2002	June 2002	July 2002	Aug. 2002	Sept. 2002	Oct. 2002	Nov. 2002	Dec. 2002	Jan. 2003	Feb. 2003	Mar. 2003	Apr. 2003	May 2003	June 2003	July 2003	Aug. 2003	Sept. 2003	Oct. 2003	Nov. 2003	Dec. 2003	Jan. 2004	Feb. 2004	Mar. 2004	Apr. 2004	May 2004	June 2004	July 2004	Aug. 2004	Sept. 2004	Oct. 2004	Nov. 2004	Dec. 2004	Jan. 2005	Feb. 2005	Mar. 2005	Apr. 2005	May 2005	June 2005	July 2005	Aug. 2005	Sept. 2005	Oct. 2005	Nov. 2005	Dec. 2005	Jan. 2006	Feb. 2006	Mar. 2006	Apr. 2006	May 2006	June 2006	July 2006	Aug. 2006	Sept. 2006	Oct. 2006	Nov. 2006	Dec. 2006
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1.  $\text{C}_2\text{H}_5\text{Br} + \text{C}_2\text{H}_5\text{MgBr} \rightarrow \text{C}_2\text{H}_5\text{C}_2\text{H}_5 + \text{MgBr}_2$   
2.  $\text{C}_2\text{H}_5\text{Br} + \text{C}_2\text{H}_5\text{MgBr} \rightarrow \text{C}_2\text{H}_5\text{C}_2\text{H}_5 + \text{MgBr}_2$   
3.  $\text{C}_2\text{H}_5\text{Br} + \text{C}_2\text{H}_5\text{MgBr} \rightarrow \text{C}_2\text{H}_5\text{C}_2\text{H}_5 + \text{MgBr}_2$   
4.  $\text{C}_2\text{H}_5\text{Br} + \text{C}_2\text{H}_5\text{MgBr} \rightarrow \text{C}_2\text{H}_5\text{C}_2\text{H}_5 + \text{MgBr}_2$   
5.  $\text{C}_2\text{H}_5\text{Br} + \text{C}_2\text{H}_5\text{MgBr} \rightarrow \text{C}_2\text{H}_5\text{C}_2\text{H}_5 + \text{MgBr}_2$   
6.  $\text{C}_2\text{H}_5\text{Br} + \text{C}_2\text{H}_5\text{MgBr} \rightarrow \text{C}_2\text{H}_5\text{C}_2\text{H}_5 + \text{MgBr}_2$   
7.  $\text{C}_2\text{H}_5\text{Br} + \text{C}_2\text{H}_5\text{MgBr} \rightarrow \text{C}_2\text{H}_5\text{C}_2\text{H}_5 + \text{MgBr}_2$   
8.  $\text{C}_2\text{H}_5\text{Br} + \text{C}_2\text{H}_5\text{MgBr} \rightarrow \text{C}_2\text{H}_5\text{C}_2\text{H}_5 + \text{MgBr}_2$   
9.  $\text{C}_2\text{H}_5\text{Br} + \text{C}_2\text{H}_5\text{MgBr} \rightarrow \text{C}_2\text{H}_5\text{C}_2\text{H}_5 + \text{MgBr}_2$   
10.  $\text{C}_2\text{H}_5\text{Br} + \text{C}_2\text{H}_5\text{MgBr} \rightarrow \text{C}_2\text{H}_5\text{C}_2\text{H}_5 + \text{MgBr}_2$

1. *THE VALUE OF A FIRM'S GOODWILL* BY J. H. VAN DER VLIET, 101  
2. *THE VALUE OF A FIRM'S GOODWILL* BY J. H. VAN DER VLIET, 101  
3. *THE VALUE OF A FIRM'S GOODWILL* BY J. H. VAN DER VLIET, 101  
4. *THE VALUE OF A FIRM'S GOODWILL* BY J. H. VAN DER VLIET, 101  
5. *THE VALUE OF A FIRM'S GOODWILL* BY J. H. VAN DER VLIET, 101  
6. *THE VALUE OF A FIRM'S GOODWILL* BY J. H. VAN DER VLIET, 101  
7. *THE VALUE OF A FIRM'S GOODWILL* BY J. H. VAN DER VLIET, 101  
8. *THE VALUE OF A FIRM'S GOODWILL* BY J. H. VAN DER VLIET, 101  
9. *THE VALUE OF A FIRM'S GOODWILL* BY J. H. VAN DER VLIET, 101  
10. *THE VALUE OF A FIRM'S GOODWILL* BY J. H. VAN DER VLIET, 101

[illegible][illegible][illegible]











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||||| 181 VSVQGLIYKAAFGCTDIKACMLDKNTSIFVSWATACVVTTSCTIISYPLTVPRRM 240
Q7 233 MMGSRKSALEIYATSTVDSHPYIFPEGCKAFKFAWNSVNLGFMGAPVLYLYFLKKVI 298
DB 241 MMGSRKSALEIYATSTVDSHPYIFPEGCKAFKFAWNSVNLGFMGAPVLYLYFLKKVI 300

RESULT 12
ADT_CHLKE
ID ADT_CHLKE STANDARD: PKT: 339 AA.
AC 031632; 1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DI 01-JUL-1993 (Rel. 36, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
OS Chlorella kessleri.
OC Eukaryota, Viridiplantae, Chlorophyta, Trebouxiophyceae, Chlorellales,
Chlorrellaceae, Chlorella.
CX NCBI_TaxID:3074;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:92084708; PubMed:1748677;
FA Hilgarth C., Sauer N., Tanner W.;
FT "Glucose increases the expression of the ATP/ADP translocator and the
glyceroldehyde-3-phosphate dehydrogenase genes in Chlorella.";
FL J. Biol. Chem. 266:2404-2407(1991).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
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or send an email to license@isb-sib.ch)
EMBL: M76669; AAA33027.1;
PIR: A41677; A41677.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PS00226; MITOCARPIER.
DR PROSITE: PS00215; MITOC_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 45 62 1 (POTENTIAL).
FT TRANSMEM 108 126 2 (POTENTIAL).
FT TRANSMEM 151 168 3 (POTENTIAL).
FT TRANSMEM 209 228 4 (POTENTIAL).
FT TRANSMEM 248 265 5 (POTENTIAL).
FT TRANSMEM 304 322 6 (POTENTIAL).
FI SEQUENCE 339 AA; 3606 MW; 5477954333942 CRC64;
Query Match 63.4%; Score 978; DB 1; Length 339;
Best Local Similarity 96.9%; Pied. No. 1; 1e-70;
Matches 198; Conservation 26; Mismatches 64; Indels 8; Gaps 5;
Q7 C ISFAPR: A5LAAATSKTAVAFIEVFLIYQVCHAKKQIADK--QYKGIYGVIPRK 63
DB 233 MAIVFT: A3GTAGALSKTAVAFIPVFLIYQVCHAKKQIADK--QYKGIYGVIPRK 98
Q7 64 SGVISEWENLANVIRFETQALNEAFKPKYQIQLGVGVYVHFWPFPAGNLASGAA 123
DB 63 FGCVASFWGRLANVIRFETQALNEAFKPKYQIQLGVGVYVHFWPFPAGNLASGAA 157
Q7 124 GA,CHGVTVTGLAFARLANVWCKSFIFPFPPGLGLCLVITKSGVIGLQVDFSVVQ 183

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RESULT 11
ADT_ANOCA
ID ADT_ANOCA STANDARD: PRI: 301 AA.
AC Q27238;
DT 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 01-NOV-1997 (Rel. 35, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
translocator) (ANT).
OS Anopheles gambiae (African malaria mosquito)
OC Eukaryota, Metazoa, Arthropoda, Insecta, Diptera, Nematocera,
Insecta, Pterygota, Neoptera, Endopterygota; Diptera: Nematocera;
OC Culicoidae, Anophelinae.
OX NCBI_TaxID 7145;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN:G3;
RX MEDLINE:94348635; PubMed:8069414;
FA Beard C.B., Crews-Owen A.E., Kumar V.K., Collins F.H.;
FT "A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles
gambiae.";
FL Insect Mol. Biol. 3:35-40(1994).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY)
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY
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or send an email to license@isb-sib.ch)
EMBL: U14618; AAR04104.1;
EMBL: U14617; AAR04105.1;
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PS00226; MITOCARPIER.
DR PROSITE: PS00215; MITOC_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 14 31 1 (POTENTIAL).
FT TRANSMEM 75 93 2 (POTENTIAL).
FT TRANSMEM 119 136 3 (POTENTIAL).
FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 216 233 5 (POTENTIAL).
FT TRANSMEM 275 293 6 (POTENTIAL).
FI SEQUENCE 301 AA; 32853 MW; 40046179690A08B CRC64;
Query Match 78.0%; Score 1204; DB 1; Length 301;
Best Local Similarity 77.7%; Pied. No. 7; 5e-100;
Matches 233; Conservation 23; Mismatches 42; Indels 1; Gaps 1;
Q7 1 PFDA: LSPADPLACGLAAATSPVAFIPVFLIYQVCHAKKQIADKQYKGIYGV 58
DB 1 MKKAGT: GKAKDPLAGLAAATSPVAFIPVFLIYQVCHAKKQIADKQYKGIYGV 60
Q7 63 QYKGIYGVIPRK 63
DB 61 VRIHQGGIGAFWRGRLANVIRFETQALNEAFKPKYQIQLGVGVYVHFWPFPAGNLASGAA 123
Q7 119 SGCAAGATSLGVVFLDIAKLAAYVGRSGTERTFSGLGGLGVLPITYSGDIPGLQGES 178
DB 121 SGCAAGATSLGVVFLDIAKLAAYVGRSGTERTFSGLGGLGVLPITYSGDIPGLQGES 180
Q7 179 VSVQGLIYKAAFGCTDIKACMLDKNTSIFVSWATACVVTTSCTIISYPLTVPRRM 240

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PRINTS: PF00926; MITOCH\_CARRIER.  
DR PROSITE: PS00215; MITOCH\_CARRIER. 2  
FW Mitochondrial inner membrane; Repeat; Transmembrane; Transport.  
FT TRANSMEM 12 29 1 (POTENTIAL).  
FT TRANSMEM 74 92 3 (POTENTIAL).  
FT TRANSMEM 116 143 3 (POTENTIAL).  
FT TRANSMEM 179 197 4 (POTENTIAL).  
FT TRANSMEM 217 224 5 (POTENTIAL).  
FT TRANSMEM 273 291 6 (POTENTIAL).  
SQ SEQUENCE 308 AA: 352x MW: 34770 Da: 777x 10. Gaps 308.  
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Best Local Similarity 51.8%; Pred. No. 20-617.  
Matches 157 Conservative 56; Mismatches 81; Indels 10; Gaps 5;  
27 1 MTFDAISAFKELAGLAAIAISKTAFAVAFERVELLQVQ-HASKQIAADKQVGLVDCIV 59  
DB 1 MAFLELHFWGLAELAAVAFATAAATPPEVTLVQWQPMKQCPASPPGICPEPV 60  
QY 60 KICKQGVLSKRWKGLAHVKEELQANAFELAAVAFERVELLQVQWYVAFANIAS 119  
DB 61 RIVREGEFSLWPGNTANVIRVFLQANAFERKEMF GENKREYKWKWFAQNMAS 119  
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DB 119 AGAAATAGVGLSTVGLATKATKELAAKAAVFGVQVPLVTVVQVTKTASDGLA 178  
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DB 176 GAVVAVGLITPAVAVVGVVQVQAG MPEPKNTHIVVQVMIAGTVTAVAGVSY 235  
QY 235 KAMMLSEKCAVIMTCTVTPVWPKTTPPEQKAPKCAKMSVILPQWCAFLVIV 295  
DB 235 LEMKTSV GSAVPTKSSVTHLELVKNEHNSLEFASANILRAVAGVAGVDC 295  
QY 296 KVI 248  
DB 296 VIL 208  
RESULT 15  
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AC Q09186;  
DT 01-Nov-1997 (Rel. 35, Created)  
DT 01-Nov-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenosine nucleotide  
DE Translocator) (ANT).  
GN ANT [K035530.100].  
OS Schizosaccharomyces pombe (Drosophila yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycotales; Schizosaccharomycetaceae;  
OC Schizosaccharomyces.  
QY Ant-1997 1846.  
RN SEQUENCE FROM N.A.  
RC STRAIN 972.  
RX MEDLINE 97203, PubMed 967601P.  
KA Conzin N., Trezequet V., Saux A.L., Languin G.J.M.,  
KA "Cloning of the gene encoding the mitochondrial adenine nucleotide  
KA carrier of Schizosaccharomyces pombe by functional complementation in  
PT Schizosaccharomyces cerevisiae".  
RL Gene 171:113-117(1996).  
RN SEQUENCE FROM N.A.  
RC STRAIN 972.  
RX MEDLINE-21848401; PubMed-11859360;  
RA Wood V., Gwilliam P., Bagdikian M.A., Lyne M., Lyne E., Stewart A.,  
RA Staden R., Post N., Hargreaves J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown E., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor A., Cronin A., Davis P., Bellwell T., Fraser A.,  
RA Gentles S., Gobie A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

























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OM protein - protein search using sw model

Run on: January 01, 2003, 11:15:30, Search time: 18 seconds  
(without alignments)  
584,535 million cell updates/sec

Title: US-09-185-904A 33

Perfect score: 1543

Sequence: 1 MTPQATSEAFALSLKSLAAAL (PROMOTIVIN) REF: 758

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262571 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DE seq length: 0

Maximum DE seq length: 2000000000

Post-processing: Minimum Match 34

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:

- 1: Sequence 10, Application US/08961871
- 2: Sequence 10, Application US/08961871
- 3: Sequence 10, Application US/08961871
- 4: Sequence 10, Application US/08961871
- 5: Sequence 10, Application US/08961871
- 6: Sequence 10, Application US/08961871

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total sequence distribution

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1412	91.5	298	3	Sequence 10, Appl
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3	1412	91.5	298	3	Sequence 10, Appl
4	1412	91.5	298	3	Sequence 10, Appl
5	1412	91.5	298	3	Sequence 10, Appl
6	1412	91.5	298	3	Sequence 10, Appl
7	1412	91.5	298	3	Sequence 10, Appl
8	1412	91.5	298	3	Sequence 10, Appl
9	1412	91.5	298	3	Sequence 10, Appl
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25	1412	91.5	298	3	Sequence 10, Appl
26	1412	91.5	298	3	Sequence 10, Appl
27	1412	91.5	298	3	Sequence 10, Appl

Sequence 37, Appl  
Sequence 37, Appl  
Sequence 37, Appl  
Sequence 37, Appl  
Sequence 4, Appl  
Sequence 1, Appl  
Sequence 56, Appl  
Sequence 56, Appl  
Sequence 56, Appl  
Sequence 19, Appl  
Sequence 15, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 6, Appl  
Sequence 10, Appl  
Sequence 142, App

## ALIGNMENTS

RESULT 1  
US-08-961-871-10  
Sequence 10, Application US/08961871  
Patent No. 6013858  
GENERAL INFORMATION:  
APPLICANT: Wallace, Douglas C.  
APPLICANT: Graham, Brett H.  
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine  
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods  
NUMBER OF SEQUENCES: 11  
REFERENCE SEQUENCE: 11  
ADDRESS: Greenlee, Winner and Sullivan, P.C.  
STREET: 5370 Manhattan Circle, Suite 201  
CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303  
COMPUTER REARABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: P-10S/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/961,871  
FILING DATE: 31-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/040,017  
FILING DATE: 01-NOV-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Donna M.  
REGISTRATION NUMBER: 33,878  
REFERENCE/REFET NUMBER: 78-66  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8080  
INFORMATION FOR SPO ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 498 amino acids  
TYPE: amino acid  
TOPOLGY: linear  
MOLECULE TYPE: protein  
US-08-961-871-10

Query Match 91.5% Score 1412 DB 3 Length 298

Best Local Similarity 88.6% Pred No 2 Seq 151

Matches 264 Conservative 19 Mismatches 15 Indels 0 Gaps 0

67 1 MTPQATSEAFALSLKSLAAALGVPIERVKLLIQVHASKQIAADQYKGIIVDCIVR 60





[illegible]







STRAND-NESS: single  
Topology: unknown  
US-08-946-719A-51

Query Match 16.2% Score 250.5; DB 3; Length 309;  
Best Local Similarity 24.3%; Pred. No. 4.9e-20;  
Matches 71; Conservative 53; Mismatches 146; Indels 25; Gaps 8

Q7 12 FLAAGTAAAKSTAVAPTEPVKIIQGHASH--GIIAADKQYKQIVGVIPKPGQVI 68  
Db 17 FLGATTAACIADLITFLDIAVVPQIUGSGGQIVPRTVSAGYQVMTILIMVTEGPR 76  
Q7 19 FFWHLAHVLEYELLALGAEETPTPTVAVFETQWYFACHASSAGACATSE 128  
Db 77 SLVAGAGAGKQASLASELITLQVAKETKQSIHAE TSSSLASTGALAV 131  
Q7 129 GVVVLEKARFLAALVCKSTETETETETETETETETETETETETETETETET 148  
Db 132 AVAGVLLVAVVPLLA APAGVLLVAVVPLLA APAGVLLVAVVPLLA APAGVLLVAVVPLLA 153  
Q7 192 AAYGVVETAT -CHPMPYVTVVWQWPAQVTVAVAGVSVSYHTTVVPPPMQGS 242  
Db 191 GAVLVITVLLQALKEALKEALKEALKEALKEALKEALKEALKEALKEALKEAL 243  
Q7 243 GPKCADIMVTCTVCPKIPFDEGKKAFFKGAWSNVIR-GMGGAFVIVLYDELKVI 298  
Db 244 RALGCTSSAGKALIMLALGCTPAITETMIEFLGSEWVVMFVTEGAL 308

RESULT 14

US-08-775-009-33  
Sequence 33, Application US/08775009  
Patent No. 5935783  
GENERAL INFORMATION:  
APPLICANT: Gonda, Weillan  
APPLICANT: Emanuel, Beverly S.  
APPLICANT: Budarf, Marcia L.  
APPLICANT: Roe, Bruce  
TITLE OF INVENTION: Rn. 535783el Genes Mapping to the Digestion and  
TITLE OF INVENTION: Villoradiotaxial Syndrome Minimal Critical Region  
NUMBER OF SEQUENCES: 45  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Weillan, Robert, Fort. Monmouth, NJ 08064  
ADDRESS: No. 5935783, US  
Street: One Liberty Place 46th floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER RELEASABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08775009  
FILING DATE: 27-DEC-1996

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Trujillo, Doreen Yalko  
REGISTRATION NUMBER: 357719  
REFERENCE/POCKET NUMBER: CH-0661  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 311 amino acids  
TYPE: amino acid  
STRAND-NESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-775-009-33

Query Match 16.2% Score 250.5; DB 2; Length 311;  
Best Local Similarity 27.6%; Pred. No. 4.9e-20;  
Matches 84; Conservative 53; Mismatches 135; Indels 27; Gaps 8;

Q7 10 PPTAGTAAATSTAVAPTEPVKIIQGHASH--GIIAADKQYKQIVGVIPKPGQVI 69  
Db 23 KALLAGTAAATSTAVAPTEPVKIIQGHASH--GIIAADKQYKQIVGVIPKPGQVI 82  
Q7 75 LKALHAGVLEAFETCALREA FFDYFQGLLEGGV-KHTQFWFYFACNLAACACAT 125  
Db 84 LYPALSLIWCILKAANVPCOMFEELSMMFDAQCPLOSP-----PGLLOGCAGVAE 135  
Q7 129 SLGVVPLDAPTEPIADWQKSTETPTPTVAVFETQWYFACHASSAGACATSE 186  
Db 135 AVVVVCPMETVVKVFIHD--QTSNPKTGTGFFHVFVREGIGKGTGGLTATVTKQGS 193  
Q7 181 ASAYELVYI-TAKGMLFUGFHIILVVSMMIACITVAVAGVSVSYHTTVVPPPMQGS 242  
Db 194 NOALRPFVMTSLRWY-QGDNPNKPMNLIITGVGAVAGAAVSFENFLDVLITRMOGLE 252  
Q7 243 GPKCADIMVTCTVCPKIPFDEGKKAFFKGAWSNVIR-GMGGAFVIVLYDELKVI 298  
Db 253 AHZ-----VENTIDGSGVLLKNGEKA-FYKGTVPRLGRVCLDVAIVFYDIYDEWKL 304

RESULT 15

US-08-937-466-4  
Sequence 4, Application US/08937466  
Patent No. 5846779  
GENERAL INFORMATION:  
APPLICANT: Zhang, Ning  
APPLICANT: Amaral, M. Catherine  
APPLICANT: Chen, Jin-Long  
TITLE OF INVENTION: UCP3 Genes  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 75 DENISE DRIVE  
CITY: HILLSBOROUGH  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94010  
COMPUTER RELEASABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/937.466  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/POCKET NUMBER: 197-009  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 343-4341  
TELEFAX: (650) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 amino acids  
TYPE: amino acid  
STRAND-NESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-937-466-4

Query Match 15.9% Score 245; DB 3; Length 432;  
Best Local Similarity 26.8%; Pred. No. 3.4e-19;  
Matches 79; Conservative 50; Mismatches 144; Indels 22; Gaps 8;

Q7 12 FLAAGTAAAKSTAVAPTEPVKIIQGHASH--GIIAADKQYKQIVGVIPKPGQVI 71













APPLICANT: Sherman, Amir  
 APPLICANT: Silva, Jeff  
 APPLICANT: Summers, Eric  
 TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi  
 FILE REFERENCE: 109272.147  
 CURRENT APPLICATION NUMBER: US 09/734,569  
 PRIOR FILING DATE: 2001-03-07  
 PRIOR APPLICATION NUMBER: US 09/487,558  
 PRIOR FILING DATE: 2000-01-19  
 PEAR APPLICATION NUMBER: US 60/160,587  
 PRIOR FILING DATE: 1997-10-20  
 NUMBER OF SEQ ID NOS: 440  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 252  
 LENGTH: 318  
 TYPE: PRT  
 ORGANISM: *Aspergillus niger*

US-09-801-368-252

Query Match 46.18% Score 740.5; DB 10; Length 318;

Best Local Similarity 53.76%; Pred No. 9; Mismatches 86; Indels 0; Gaps 5;

Matches 157; Conservation 44; Mismatches 84; Indels 0; Gaps 5;

QY 7 SPARKLEAGGIAAATKAVAPTEPVKLLIQVQ-HASKQIAADKUYKGLVUC-VKLPKEQ 65

DB 22 NLLQFLNGCVSAAVKTAASVLEPVKLLIQVQEMVFGTLDPKYAGILDKPKPTAG 81

QY 56 CVLSFWENLANVPEYPTQALNFAKPKYK-PIVGVKHTDTPWYFACNLSGCAAGA 125

DB 82 VVLSFWENLANVPEYPTQALNFAKPKYK-PIVGVKHTDTPWYFACNLSGCAAGA 145

QY 126 TSLCTVYVLDFAETPLAADV---GKSTPEPPFGIGVIVKLTGSPGIGLYGFSVSQ 183

DB 140 LSLVYVLDFAETPLAADV---GKSTPEPPFGIGVIVKLTGSPGIGLYGFSVSQ 199

QY 183 GTTHPAAYTGVYVTKG-MLEPKNT-IVVSWKIAOTVATVAGVSVYPTPPPMQ 241

DB 253 GTTHPAAYTGVYVTKG-MLEPKNT-IVVSWKIAOTVATVAGVSVYPTPPPMQ 272

QY 242 SCRGASIMTGVTCWPKIPPPDEGGKAPFKGANSVLRMGAGVLYDE K 295

DB 323 SCGA- VKNCEMFAKQILAKPKAKTPEKAGANLPAVAGAGVISQYD Q 373

RESULT 11

US-09-734-569-170

Sequence 170; Application US/09734569

Patent No. US20020064816A1

GENERAL INFORMATION:

APPLICANT: Renz, Andreas

APPLICANT: Erhardt, Thomas

APPLICANT: Reindl, Andreas

APPLICANT: Citrus, Petra

APPLICANT: Bischoff, Friedrich

APPLICANT: Frank, Markus

APPLICANT: Freund, Annette

APPLICANT: Duwenig, Elke

APPLICANT: Schmidt, Ralf-Michael

APPLICANT: Reski, Ralf

TITLE OF INVENTION: Methods for the synthesis of carbohydrates

FILE REFERENCE: BASF SAE 132-99-08

CURRENT APPLICATION NUMBER: US/09734569

CURRENT FILING DATE: 2001-03-24

PRIOR APPLICATION NUMBER: US 60/171,101

PRIOR FILING DATE: 1997-12-15

NUMBER OF SEQ ID NOS: 181

SOFTWARE: PatentIn Ver. 2.1/wordedirect 6.1

SEQ ID NO 170

LENGTH: 386

TYPE: PRT

ORGANISM: *Physcomitrella patens*

US-09-734-569-170

Query Match 48.6% Score 749.5; DB 10; Length 386;

Best Local Similarity 53.4%; Pred No. 9; Mismatches 84; Indels 0; Gaps 5;

Matches 157; Conservation 44; Mismatches 84; Indels 0; Gaps 5;

QY 7 SPARKLEAGGIAAATKAVAPTEPVKLLIQVQ-HASKQIAADKUYKGLVUC-VKLPKEQ 65

DB 84 STPTDLMGCVSAAVKTAADPIERVKLLIQVQEMVFGTLDPKYAGILDKPKPTAG 143

QY 56 CVLSFWENLANVPEYPTQALNFAKPKYK-PIVGVKHTDTPWYFACNLSGCAAGA 125

DB 144 GMSKWRGNANVRYFTQALNFAKPKYK-PIVGVKHTDTPWYFACNLSGCAAGA 202

QY 126 TSLCTVYVLDFAETPLAADV---GKSTPEPPFGIGVIVKLTGSPGIGLYGFSVSQ 182

DB 293 SLLVYVLDFAETPLAADV---GKSTPEPPFGIGVIVKLTGSPGIGLYGFSVSQ 262

QY 183 GTTHPAAYTGVYVTKG-MLEPKNT-IVVSWKIAOTVATVAGVSVYPTPPPMQ 241

DB 253 GTTHPAAYTGVYVTKG-MLEPKNT-IVVSWKIAOTVATVAGVSVYPTPPPMQ 272

QY 242 SCRGASIMTGVTCWPKIPPPDEGGKAPFKGANSVLRMGAGVLYDE K 295

DB 323 SCGA- VKNCEMFAKQILAKPKAKTPEKAGANLPAVAGAGVISQYD Q 373

RESULT 12

US-09-925-301-1459

Sequence 1129; Application US/09025301

Patent No. US2002005208A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09025301

CURRENT FILING DATE: 2001-08-10

SEQUENCE APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

FEINTE APPLICATION NUMBER: 650124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1459

LENGTH: 132

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (115)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (123)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (126)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (129)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-301-1459

Query Match 33.6% Score 518; DB 10; Length 132;

Best Local Similarity 36.3%; Pred No. 9; Mismatches 4; Indels 0; Gaps 0;

Matches 133; Conservation 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 VTFQALSPAKDFLACCTAAATSPATAVPIEPVKLLIQVQEMVFGTLDPKYAGILDKPKPTAG 60

DB 26 MTFQALSPAKDFLACCTAAATSPATAVPIEPVKLLIQVQEMVFGTLDPKYAGILDKPKPTAG 85

QY 61 TPKEQGVLSFWENLANVPEYPTQALNFAKPKYK-PIVGVKHTDTPWYFACNLSGCAAGA 107

DB 86 TPKEQGVLSFWENLANVPEYPTQALNFAKPKYK-PIVGVKHTDTPWYFACNLSGCAAGA 132



```
? SEQ ID NO: 2
? LENGTH: 177
? TYPE: PRT
? ORGANISM: Homo sapiens
US-09-777-921A-2

Query Match      23.8%   Score 568   DB 10   Length 477
Best Local Similarity 32.7%   Prod. No. 18-29
Mismatch 47   Occurrence 60   Mismatch 112   Indels 22   Gaps 10

QY 10 KTLALAEIAAIAKSTAVAEIEPVKGLAQVQIAKFKQAAGKQYKQIVGIVFIRKQGVLS 69
DB 196 KQVLAAGIACAGAVSTSTAPDPIKIMQV-HGSK---SDGM-NIFGDFQGVKGGIIPS 249
QY 70 FWRNLANVIFPPTTAAINFAKPTFTFTLGLGVTFHIGRWPFACNLASGAGATSLC 129
DB 250 LWRNGINVIKIAPEIAVFWAYEQVKEELLEEGQKIGTGERFISGM-----AGATACT 304
QY 130 FVGLIGFARGLAAGAKSTETFEFFKGLNFTAKTKESDRIPTIYQGFVSVDGIIIDYRA 189
DB 305 FLYPMVMMKIRLA--VKKIG---QYSNTYDARKIKHFGIGAFYKGVVFNLLGIIPYAG 359
QY 190 AYGVYELAK---GMLIFTEHCHVVSWHIAGIVTAVAGVVVSYPFLIVFEFMMMSGE 244
DB 360 IDAVVELLSYWLDFNFKDSVMPGVNVLGGALSSDGGVASYPLALVPTPMQACAPL 419
QY 245 KTAELMYETIVTQWPTFEFFQKFAFEKZAHN---VLRGMGZAFVLVLYDELEKVI 298
DB 420 EGNQQL--NNAVGLPRITSKEGIDCLYFGITPNEFMKVLPAVGISY--VVYENMKQTL 472
```

Search completed: January 2, 2003, 14:51:08  
Job time : 15 secs



GenCore version 5.1.3  
Copyright (c) 1993-2003 CompuGen Ltd.

Query protein: protein search, using sw model

Run on: January 3 10:31:15, 2003  
(without alignments)  
1860.668 Million cell updates, 300

Title: US-09-185-904a-33  
Perfect score: 1543  
Sequence: 1 MIEQATSFARLEIAKIDAA.....LECMGSAFLVILNEERKVI 298

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 67586

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_oruanelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_protist.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacterioph.\*
- 17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match	Length	DE	ID	Description
1	1451	54.7	299	5	095VX4	095VX4	095VX4
2	1447	52.5	298	5	095VX4	095VX4	095VX4
3	1421	52.1	298	11	095VX4	095VX4	095VX4
4	1418	91.3	298	11	095VX4	095VX4	095VX4
5	1409	91.3	298	13	095VX4	095VX4	095VX4
6	1406	91.1	298	13	095VX4	095VX4	095VX4
7	1402	90.9	298	13	095VX4	095VX4	095VX4
8	1400	84.3	299	5	095VX4	095VX4	095VX4
9	1397	81.6	299	5	095VX4	095VX4	095VX4
10	1254	81.3	299	5	095VX4	095VX4	095VX4
11	1245	80.1	300	5	095VX4	095VX4	095VX4
12	1187	77.0	298	5	095VX4	095VX4	095VX4
13	1183	76.7	298	5	095VX4	095VX4	095VX4
14	1176	76.2	304	5	095VX4	095VX4	095VX4
15	1172	73.7	303	7	095VX4	095VX4	095VX4
16	1119	72.5	315	4	095VX4	095VX4	095VX4

17	1041	67.5	312	5	021132	021132	021132
18	1039	67.3	313	5	021132	021132	021132
19	1038	67.3	300	5	045855	045855	045855
20	996	64.5	309	5	097470	097470	097470
21	993.5	64.4	300	5	001813	001813	001813
22	993	64.4	300	5	017437	017437	017437
23	973.5	62.1	318	5	09BJ36	09BJ36	09BJ36
24	946.5	61.3	307	5	09X522	09X522	09X522
25	944	61.2	321	5	025632	025632	025632
26	943	61.1	321	5	020236	020236	020236
27	821	61.6	170	5	02X529	02X529	02X529
28	778.5	60.5	305	4	09JRM1	09JRM1	09JRM1
29	764	49.5	326	5	091270	091270	091270
30	760	49.3	307	5	075286	075286	075286
31	759	49.0	303	3	074360	074360	074360
32	756.5	49.0	305	5	018368	018368	018368
33	753	49.8	307	5	025647	025647	025647
34	747	49.4	306	3	073754	073754	073754
35	744	48.2	388	10	049875	049875	049875
36	743	48.2	379	10	049447	049447	049447
37	743	48.2	386	10	033767	033767	033767
38	734	47.6	331	10	041628	041628	041628
39	731.5	47.4	305	3	09P876	09P876	09P876
40	731	47.4	317	5	09N647	09N647	09N647
41	728.5	47.2	305	3	09P875	09P875	09P875
42	724.5	47.0	308	3	08JFA7	08JFA7	08JFA7
43	688.5	44.8	330	10	04PM86	04PM86	04PM86
44	691.5	44.7	298	5	021804	021804	021804
45	653.5	42.4	262	10	05AVT5	05AVT5	05AVT5

ALIGNMENTS

RESULT 1

Q8SQH5	Q8SQH5	PRELIMINARY:	PRT:	298 AA.
ID	Q8SQH5			
AC	Q8SQH5			
DT	01-JUN-2002 (TrEMBLrel. 21, Created)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)			
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)			
DR	Adjuvant nucleoside translocator 2.			
OS	pos rufous (rodent)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovina; Bovidae;			
OC	Povidae; Bovinae; Bos			
OX	NCBI TaxID=9913;			
RN	[1]			
RU	SEQUENCE FROM N.A.			
RA	Yoshida K., Shiohara Y., Tanaka K., Terada H.			
RT	"Structural properties of mammalian mitochondrial ADP/ATP carriers: identification of possible amino acids that determine functional differences in its isoforms."			
RL	Mitochondrion 1:371-379(2002).			
DR	EMBL: AB065433; BAB84673.1; ...			
SQ	SEQUENCE 298 AA: 32555 MW: 686978987P7400 QP644:			

Query Match	94.0%	Score 1451;	FR 6;	Length 298;
Best Local Similarity	92.0%	Prod No. 50119;		
Matches	273;	Conservative	13;	Mismatches 10;
				Indels 0;
				Gaps 0;
Q7	1 MTEQISAPFPLAGIAAAISKIAVPIFVRLIIQVQASQIAADQYKGIIVICIVR	60		
DB	1 MTPAAVSPAKDPAQGVAAAISKIAVPIFVRLIIQVQASQIAADQYKGIIVICIVR	60		
Q7	61 LIIEGVSEFSENLARVFEETCALREAFKPFVYVTFVTKHFFQWPFYAGRIASG	120		
DB	61 LIIEGVSEFSENLARVFEETCALREAFKPFVYVTFVTKHFFQWPFYAGRIASG	120		
Q7	121 GAADAISCEVVVTFAPTFIAADVVSCHIFFPFPPIQDTIVITKSDTPTPLVQ2PFSV	180		
DB	121 GAADAISCEVVVTFAPTFIAADVVSCHIFFPFPPIQDTIVITKSDTPTPLVQ2PFSV	180		













Phylogeny: Phyllophoridae: Phyllophoridae

CC  
CX  
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CZ  
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DB  
DC  
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DG  
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JN  
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